

## ABSTRACT

5        Generation of longer cDNA fragments from SAGE tags for gene identification  
(GLGI) is disclosed. This method converts SAGE tags, which are about 10 base pairs in  
length, into their corresponding 3' cDNA fragments covering hundred bases. This added  
information provides for more accurate genome-wide analysis and overcomes the  
inherent deficiencies of SAGE. The generation of longer cDNA fragments from isolated  
and purified protein fragments for gene identification is also disclosed. This method  
converts a short amino acid sequence into extended versions of the DNA sequences  
10        encoding the protein/protein fragment and additional 3' end sequences of the gene  
encoding the protein. This additional sequence information allows gene identification  
from purified protein sequences. The invention also provides a high-throughput GLGI  
procedure for identifying genes corresponding to a set of unidentified SAGE tags.